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        M P S R C H

                                                        (TM)
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Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn   n.a. - n.a. database search, using Smith-Waterman algorithm

on: Thu Aug 21 10:01:25 1997; MasPar time 180.55 Seconds
                                          832.142 Million cell updates/sec

Tabular output not generated.

Title:
Description: >US-08-469-637A-1
Perfect Score: (1-1527) from US08469637A.seq
N.A. Sequence: 1527
Comp: 1 CGCCCAGCCCCGCGCCTCCAA.............TTCAACTGGAAAAAAAAAA 1527
                     GCGGGTCGCGCGCGGCGGAGGTT..........AAGTTGACCTTTTTTTTTTTT

Scoring table: TABLE default
                   Gap 6

Nmatch STD :   Dbase 0; Query 0

Searched: 134151 seqs, 49196315 bases x 2

Post-processing: Minimum Match 0%
                   Listing first 45 summaries

Database: n-geneseq27
                   1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
                   8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
                   14:part14 15:part15 16:part16 17:part17 18:part18
                   19:part19 20:part20 21:part21 22:part22 23:part23
                   24:part24 25:part25 26:part26 27:part27

Statistics: Mean 9.385; Variance 5.205; scale 1.803

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES
```

| Result No. | Score | % Query Match | Length | DB | ID | Description | Pred. No. |
|---|---|---|---|---|---|---|---|
| 1 | 1204 | 78.8 | 1206 | 27 | T36685 | Osteoclastogenesis in | 0.00e+00 |
| 2 | 1200 | 78.6 | 1206 | 27 | T33165 | Mutated OCIF, OCIF-C2 | 0.00e+00 |
| 3 | 1200 | 78.6 | 1206 | 27 | T33164 | Mutated OCIF, OCIF-C2 | 0.00e+00 |
| 4 | 1200 | 78.6 | 1206 | 27 | T33162 | Mutated OCIF, OCIF-C2 | 0.00e+00 |
| 5 | 1198 | 78.5 | 1206 | 27 | T33161 | Mutated OCIF, OCIF-C2 | 0.00e+00 |
| 6 | 1198 | 78.5 | 1206 | 27 | T33163 | Mutated OCIF, OCIF-C1 | 0.00e+00 |
| 7 | 1196 | 78.3 | 1200 | 27 | T33172 | Mutated OCIF, OCIF-CL | 0.00e+00 |
| 8 | 1173 | 76.8 | 1182 | 27 | T33178 | Mutated OCIF, OCIF-CB | 0.00e+00 |
| 9 | 1052 | 68.9 | 1056 | 27 | T33173 | Mutated OCIF, OCIF-CC | 0.00e+00 |
| 10 | 1052 | 68.9 | 1083 | 27 | T33166 | Mutated OCIF, OCIF-DC | 0.00e+00 |
| 11 | 1017 | 66.6 | 966 | 27 | T33179 | Mutated OCIF, OCIF-CS | 0.00e+00 |
| 12 | 951 | 62.3 | 1080 | 27 | T33167 | Mutated OCIF, OCIF-DC | 0.00e+00 |
| 13 | 890 | 58.3 | 984 | 27 | T33171 | Mutated OCIF, OCIF-DD | 0.00e+00 |
| 14 | 816 | 53.4 | 819 | 27 | T33174 | Mutated OCIF, OCIF-CD | 0.00e+00 |
| 15 | 765 | 50.1 | 1080 | 27 | T33168 | Mutated OCIF, OCIF-CD | 0.00e+00 |
| 16 | 663 | 43.4 | 10190 | 27 | T33183 | Fragment of human OCI | 0.00e+00 |

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                            ALIGNMENTS
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17	649	42.5	1080	27	T33169	Mutated OCIF, OCIF-DC	0.00e+00
18	598	39.2	981	27	T33170	Mutated OCIF, OCIF-DD	0.00e+00
19	589	38.6	594	27	T33175	Mutated OCIF, OCIF-CD	0.00e+00
20	558	36.5	564	27	T33180	Mutated OCIF, OCIF-CB	0.00e+00
21	428	28.0	432	27	T33176	Mutated OCIF, OCIF-CC	1.12e-297
22	402	26.3	438	27	T33176	Osteoclastogenesis in	9.46e-278
23	400	26.2	465	27	T36688	Osteoclastogenesis in	3.22e-276
24	318	20.8	321	27	T33177	Mutated OCIF, OCIF-CP	1.35e-213
25	244	16.0	255	27	T33181	Mutated OCIF, OCIF-CP	1.77e-157
26	99	6.5	1047	2	Q10572	Human Natriuretic Pep	3.74e-50
27	80	5.2	1047	2	Q10572	Human Natriuretic Pep	9.70e-37
28	75	4.9	1317	27	T33182	Fragment of human OCI	2.88e-33
29	45	2.9	91	1	N81164	Oligonucleotide probe	2.87e-13
30	42	2.8	204	1	Q51746	Base substituted E.co	2.17e-11
31	39	2.6	91	9	Q51746	Oligonucleotide probe	1.52e-09
32	36	2.4	114	12	Q70465	Generic DNA sequence	9.72e-08
33	36	2.4	114	12	Q70470	Generic DNA sequence	9.72e-08
34	36	2.4	114	12	Q70469	Generic DNA sequence	9.72e-08
35	37	2.4	204	1	N81164	Base substituted E.co	2.46e-08
36	35	2.3	114	12	Q70467	Generic DNA sequence	3.80e-07
37	33	2.2	114	12	Q70468	Generic DNA sequence	5.59e-06
38	33	2.2	114	12	Q70466	Generic DNA sequence	5.59e-06
39	33	2.2	114	12	Q70467	Generic DNA sequence	5.59e-06
40	33	2.2	114	12	Q70468	Generic DNA sequence	1.47e-06
41	32	2.1	114	12	Q70473	Generic DNA sequence	2.10e-05
42	32	2.1	114	12	Q70465	Generic DNA sequence	2.10e-05
43	32	2.1	114	12	Q70469	Generic DNA sequence	2.10e-05
44	31	2.0	114	12	Q70472	Generic DNA sequence	7.78e-05
45	30	2.0	114	12	Q70466	Generic DNA sequence	2.84e-04

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RESULT     1
ID    T36685 standard; DNA; 1206 BP.
AC    T36685;
DT    22-APR-1997  (first entry)
DE    Osteoclastogenesis inhibitory factor coding sequence.
KW    Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
OS    Homo sapiens; ss.
OS    Homo sapiens.
KW
FH    Key              Location/Qualifiers
FT    sig_peptide      1..63
FT    /*tag= a
FT    /*tag= a
FT    mat_peptide      64..1203
FT    /*tag= b
FT    /label= Claim 6
PN    WO9626217-A1.
PD    29-AUG-1996.
PF    20-FEB-1996; J00374.
PF    20-FEB-1995; JP-054977.
PR    21-JUL-1995; JP-207508.
PA    (SNOW ) SNOW BRAND MILK PROD CO LTD.
PI    Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
PI    Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
DR    WPI; 96-402320/40.
DR    P-PSDB; R99924-25.
PT    DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT    for bone resorption control, esp. treatment of osteoporosis
PS    Claim 8; Page 66-67; 183pp; Japanese.
CC    This sequence encodes the full length osteoclastogenesis inhibitory
CC    factor (OCIF) of the invention. The OCIF has a molecular weight by
CC    SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-
CC    reducing conditions. The protein is adsorbed onto cation-exchangers
CC    or heparin and its activity is lowered after 10 mins at 70 deg.C or
CC    30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is
CC    useful in the control of bone resorption and therefore in the
CC    treatment and prevention of disorders of bone resorption, e.g.
CC    osteoporosis.
SQ    Sequence 1206 BP;          388 A;      284 C;      269 G;    265 T;

Query Match              78.8%;    Score 1204;  DB 27;  Length 1206;
Best Local Similarity    99.9%;    Pred. No. 0.00e+00;
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Matches 1205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      1 atgaacaacttgctgtgctgcgcgctcgtgtttctggacatctccattaagtggaccacc 60
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Qy     46 ATGAACAACAAGTTGCTGTTGCTGCGCGCTCCGTGTTTCTGGACATCTCCATTAAGTGGACCACC 105

Db     61 caggaaaacgttcctccaaagtacctcacctcattatgacgaagaaacctctcacctgttg 120
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Qy    106 CAGGAAAACGTTTCCTCCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTG 165

Db    121 tgtgacaaatgtcctctggttacctcacctaaaacaacactgtacagcaggaaagtggaagacc 180
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Qy    166 TGTGACAAAATGTCCTCTCGGTTACCTCACCTAAAACAACACTGTACAGCAGGAAAGAGACC 225

Db    181 gtgtgtgcgccccttgccctgaccacctactacacagacagcagctggcaccagtgacgagtgt 240
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Qy    226 GTGTGCGCCCCTTGCCCTGACCACTACTACACAGACAGCAGCTGGCACCAGTGACGAGTGT 285

Db    241 ctatactgcagctagcaagggcccgtgtgcgcaagggaagctgcaagtcaatccgcacc 300
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Qy    286 CTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAAGCAGTCAATCCGCACC 345

Db    301 cacaaacccgctgtgcgaatgcaaggcaaggaaggcgctacctcttgagataagagttctgcttgaaa 360
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Qy    346 CACAAACCCGCTGTGCGAATGCAAGGAAGGGCCCTACCTTGAGATAGAGTTCTGCTTGAAA 405

Db    361 cataggagctgccctcctggatttggagtggtgcaaggctggaaccccagaggacgaaataca 420
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Qy    406 CATAGGAGCTGCCCTCCTGGATTTGGAGTGGTGCAAGGCTGGAACCCCAGAGGACGAAATACA 465

Db    421 gttttgaaaaatgtgtccaagatgggttcttctctcaaaatgaagagactcattaaagcaccctgt 480
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Qy    466 GTTTTGCAAAAATGTGTCCAGATGGGTTCTTCTCTCAAAATGAAGAGGCTCATCTAAAGCACCCTGT 525

Db    481 agaaaaacacacacaaattgcagtgtgtctcttcctgctaacctcagaaaaggaaatgcaaca 540
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Qy    526 AGAAAAACACACAAATTGCAGTGTCTTTGGTCTCCCTGCTAACTCAGAAAAGGAAATGCAACA 585

Db    541 cacgacaacatatgttccggaaacagtgaatccaactcaaaaaaatgtggaatagatgttacc 600
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Qy    586 CACGACAACATATGTTCCGGAAACAGTGAATCAACTCAAAAAATGTGGAATAGAATGTTACC 645

Db    601 ctgtgtgaagggaggcaattcttcttgctgttctccacaaagttcgcgcctaactgcctt 660
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Qy    646 CTGTGTGAGGGAGGCAATTCTTCACGTTTGCTGTTTCCTACAAAGTTTACGCCTAACTGCCTT 705

Db    661 agtgtcttgtagacaaatttgcctgccaccaaagtaaacgcagagagtgtagaagaggata 720
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Qy    706 AGTGTCTTGGTAGACAAATTTGCCTGGCCACCAAAGTAAACGCAGAGAGTGTAGAGGAGGATA 765

Db    721 aaaacggcaacaagctcacaagaacaagagactttccagctgctgaagttattggaaacattcaa 780
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Qy    766 AAACGGCAACACAGCTCACAAGAACAAGAGACTTTCCAGCTGCTGAAGTTATTGGAAACATCAA 825

Db    781 aacaaagacaagatagtagaagaatcatccaagaagatattgactcctgtgaaaacagc 840
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Qy    826 AACAAAGACCAAGATATAGTCAAGAAGAGNTCATCCAAGAAGATATTGACCCTGTGAAAACAGC 885

Db    841 gtgcacgcggcacattggacatgctaacctcacctgagcagcttcgtagcttgatgaa 900
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Qy    886 GTGCACGCGGCACATTGGACATCCTAACCTTGAGCAGCTTGTGTAGCTTGATGGAA 945

Db    901 agcttaccgggaaagaaagtggggacgaagacagcaattgaaaaaaacaatcaataaaggcatgcaa 960
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Qy    946 AGCTTACCGGGAAAGAAAGTGGGGAGCAGAGNAGNCAATTGAAAAAAACAATAAAAAGGCCATGCAAA 1005

Db    961 cccagtgaccagagatcctgaacgtgtcgaataaaaaaaatgggaaccaagac 1020
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Qy   1006 CCCAGTGACCAGATCCTGAAGCTGCTCAGTTTGTGTGGGCGAATAAAAAAAATGGCACCAAGAC 1065

Db   1021 accttgaaggcctaatgcacgccactaaagcactcaaagacgtacccctttcccaaaact 1080
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Qy   1066 ACCTTGAAGGGCCTAATGCACGCCACTAAAGCACTCAAAGAGAGTACCACCTTTCCCAAAACT 1125
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RESULT 2

ID T33165 standard; DNA; 1206 BP.
AC T33165;
DT 22-APR-1997 (first entry)
DE Mutated OCIF, OCIF-C23S, coding sequence.
KW Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
KW osteoporosis; ss.
OS Synthetic.
FH Key   Location/Qualifiers
FT sig_peptide   1..63
FT /tag= a
FT mat_peptide   64..1203
FT /tag= b
FT /*tag=
FT /product= OCIF-C23S
PN WO9626217-A1.
PD 29-AUG-1996.
PF 20-FEB-1996; J00374.
PR 20-FEB-1995; JP-054977.
PR 21-JUL-1995; JP-207508.
PA (SNOW) SNOW BRAND MILK PROD CO LTD.
PI Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
DR WPI; 96-402320/40.
DR P-PSDB; R99935.

CC DNA encoding osteoclastogenesis inhibitory factor protein - useful
CC for bone resorption control, esp. treatment of osteoporosis
PS Claim 39; Page 136-137; 183pp; Japanese.
CC This sequence encodes a mutated version of the full length
CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This
CC sequence encodes inhibitory factor OCIF-C23S in which the 23rd Cys
CC OCIF protein is substituted by Ser. The OCIF of the invention has a
CC molecular weight by SDS-PAGE of 60 kD under reducing conditions and
CC 120 kD under non-reducing conditions. The protein is adsorbed onto
CC cation-exchangers or heparin and its activity is lowered after 10 mins
CC at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
CC deg.C. OCIF is useful in the control of bone resorption and therefore
CC in the treatment and prevention of disorders of bone resorption, e.g.
CC osteoporosis.
SQ Sequence   1206 BP;   389 A;   285 C;   268 G;   264 T;

Query Match   78.6%;   Score 1200;   DB 27;   Length 1206;
Best Local Similarity 99.8%;   Pred. No. 0.00e+00;
Matches 1203; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db     61 caggaaaacgttcctccaaagtacctcacctcattatgacgaagaaacctctcacctgttg 60
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Qy    166 TGTGACAAAATGTCCTCTCGGTTACCTCACCTAAAACAACACTGTACAGCAGGAAAGAGACC 225

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Qy    226 GTGTGCGCCCCTTGCCCTGACCACTACTACACAGACAGCAGCTGGCACCAGTGACGAGTGT 285
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RESULT   3
ID    T33164 standard; DNA; 1206 BP.
AC    T33164;
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Left column alignment:

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Db  1246 TTATAA 1206

Qy  1201 ttataa 1206
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Qy  1186 TATCAGAAGTTATTTTTAGAAATGATAGGTAACCAGGTCCAATCACAAGTACAAAATAAAGCTGC 1245
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Qy  1141 tatcagaagttattttttagaaatgataggtaaccaggtccaatcagtacaaaataagcagc 1200
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Qy  1126 GTCACTCAGAGTCTAAAGAGAACGACCATCAGGTTCCTTCACAGTCACAAATTG 1185
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Qy  1081 gtcactcaagtcaagagacaatcagacttcttcacagttcttcacagttctttcacaatgtacaaattg 1140
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Qy  1021 accttgaaggggcacttaatgcacgcactaccacacttcccaaaact 1080
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Qy  1006 CCCAGTGACCAGATCCTGAAGCTGCTCAGTTTGTGGGGAATAAAAAATGGCGACCAAGAC 1065
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Qy   961 cccagtgaccagatcctgaagctgctctcagtttgtggcgaataaaaaatggcgaccaagac 1020
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Db   901 agcttacccgggaaagaaaaagtgggagcagagagacattgaaaaaaacaataaaggcatgcaa 960

Qy   901 agcttacccgggaaagaaaaagtgggagcagagagacattgaaaaaaacaataaaggcatgcaa 960
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Db   886 GTGCAGCGGCGGCCACATTGGACAATGCTAAACCTCAACCTTCGTAGCTTGATGGAA 945

Qy   886 GTGCAGCGGCGGCCACATTGGACAATGCTAAACCTCAACCTTCGTAGCTTGATGGAA 945
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Qy   841 gtgcagcggcacattggacaatgctaacctcaacctcgagcagcttcgtagcttgatgaa 900
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Qy   826 AACAAAGAACCAAAGATATAAGTCAAGAAGGATCATCCAAGATAATTGACCTCTGTGAAAACAGC 885
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Qy   781 aacaaagaaccaaagatatagtcaagaagatcatccaagatattgacctctgtgaaaacagc 840
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Qy   766 AAACGGCAACACAGCTCACAAGAACAGACTTTCCAAGCTGCTGAAGTTATGGAACAATCAA 825
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Qy   721 aaacggcaacacagctcacaaagaacaagacactttcacagctgctgaagttatggaacatcaa 780
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Qy   661 agtgtcttggtagacaaatttgcctggcaccaaagtaaacgcagagagtgtagaggata 720
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Qy   301 cacaaccgcgtgtgcggaatgcaaggaaggggcgctaccttgagatagagttctgcttgaaa 360
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Db   286 CTATACTGCAGCCCCGTGTGTCCAAAGGAGCTCCAAGCAGTCAAGCAGAGTGCAATCGCACC 345

Qy   286 CTATACTGCAGCCCCGTGTGTCCAAAGGAGCTCCAAGCAGTCAAGCAGAGTGCAATCGCACC 345
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Right column:

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DT   22-APR-1997  (first entry)
DE   Mutated OCIF, OCIF-C22S, coding sequence.
KW   Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
KW   osteoporosis; ss.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   sig_peptide     1..63
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FT   /*tag= b
FT   /product= OCIF-C22S
PN   WO9626217-A1.
PD   29-AUG-1996.
PF   20-FEB-1996.
PR   20-FEB-1995; JP-J00374.
PR   20-FEB-1995; JP-054977.
PR   21-JUL-1995; JP-207508.
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
PI   Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
PI   Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
DR   WPI; 96-402320/40.
DR   P-PSDB; R99934.
CC   DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT   for bone resorption control, esp. treatment of osteoporosis
PS   Claim 36; Page 135-136; 183pp; Japanese.
CC   This sequence encodes a mutated version of the full length
CC   osteoclastogenesis inhibitory factor (OCIF) of the invention. This
CC   sequence encodes OCIF-C22S in which the 22nd Cys residue in the mature
CC   OCIF protein is substituted by Ser. The OCIF of the invention has a
CC   molecular weight by SDS-PAGE of 60 kD under reducing conditions and
CC   120 kD under non-reducing conditions. The protein is adsorbed onto
CC   cation-exchangers or heparin and its activity is lowered after 10 mins
CC   at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
CC   deg.C.  OCIF is useful in the control of bone resorption and therefore
CC   in the treatment and prevention of disorders of bone resorption, e.g.
CC   osteoporosis.
SQ   Sequence 1206 BP; 389 A; 285 C; 268 G; 264 T;

Query Match 78.6%; Score 1200; DB 27; Length 1206;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 1203; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy    1 atgaacaacttgctctgtgcctgcgcgctctgttctcgtgtttctggacatctccattaagtggaccacc 60
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Qy   61 caggaaacgttctcctccaaagtacctcattatgacgagaagaaacctctctcagctgttg 120
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Db  466 GTTTGCAAAAGATGTCCAGATGGGTTCTTCTCTGCAAATGAGACGTCATCTAAAGCACCCTGT 525
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PI Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
DR WPI; 96-402320/40.
DR P-PSDB; R99932.
PT DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT for bone resorption control, esp. treatment of osteoporosis
PS Claim 30; Page 133-134; 183pp; Japanese.
CC This sequence encodes a mutated version of the full length
CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This
CC sequence encodes OCIF-C20S in which the 20th Cys residue in the mature
CC OCIF protein is substituted by Ser. The OCIF of the invention has a
CC molecular weight by SDS-PAGE of 60 kD under reducing conditions and
CC 120 kD under non-reducing conditions. The protein is adsorbed onto
CC cation-exchangers or heparin and its activity is lowered after 10 mins
CC at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
CC deg.C. OCIF is useful in the control of bone resorption and therefore
CC in the treatment and prevention of disorders of bone resorption, e.g.
CC osteoporosis.
SQ Sequence 1206 BP; 389 A; 283 C; 270 G; 264 T;

Query Match   78.6%; Score 1200; DB 27; Length 1206;
Best Local Similarity   99.8%; Pred. No. 0.0e+00;
Matches 1203; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db   1 atgaacaacttgtgctgctgcgcgtcgtgttctctgtgacactccattaaggggaacacg   60
Qy   46 ATGAACAACGTTGCTGCTGCGCGTCGTGTTCTCTGTGACAATCTCCATTAAGTGGACCACC 105

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AC T33162;

RESULT 4
ID T33162 standard; DNA; 1206 BP.
AC T33162;
DT 22-APR-1997 (first entry)
DE Mutated OCIF, OCIF-C20S, coding sequence.
KW Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
KW osteoporosis;
OS Synthetic.
FH Key   Location/Qualifiers
FT sig_peptide   1..63
FT /*tag= a
FT mat_peptide   64..1203
FT /*tag= b
FT /product= OCIF-C20S
PN WO9626217-A1.
PD 29-AUG-1996.
PF 20-FEB-1996; J00374.
PR 20-FEB-1995; JP-054977.
PR 21-JUL-1995; JP-207508.
PA (SNOW) SNOW BRAND MILK PROD CO LTD.

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Qy   1006 CCCAGTGACCAGATCCTCGAAGCTGCTCAGTTTGTTGGCGAATAAAAATGGCGACCAAGAC 1065
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Qy   1021 accttgaaggggcctaatgcacgccactcaagagacgtaccacactttcccaaaact 1080
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ID    T33161 standard; DNA; 1206 BP.
ID    T33161;
AC    T33161;
DT    22-APR-1997 (first entry)
DE    Mutated OCIF, OCIF-C19S, coding sequence.
KW    Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
KW    osteoporosis; ss.
OS    Synthetic.
FH    Key             Location/Qualifiers
FT    sig_peptide     1..63
FT    /*tag=          a
FT    mat_peptide     64..1203
FT    /*tag=          b
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PN    WO9625217-A1.
PD    29-AUG-1996.
PF    20-FEB-1996; JP00374.
PR    20-FEB-1995; JP-054977.
PR    21-JUL-1995; JP-207508.
PA    (SNOW ) SNOW BRAND MILK PROD CO LTD.
PI    Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
PI    Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
DR    WPI; 96-40320/40.
DR    P-PSDB; R99931.
PT    DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT    for bone resorption control, esp. treatment of osteoporosis
PS    Claim 27; Page 132; 183pp; Japanese.
CC    This sequence encodes a mutated version of the full length
CC    osteoclastogenesis inhibitory factor (OCIF) of the invention. This
CC    sequence encodes OCIF-C19S in which the 19th Cys residue in the mature
CC    OCIF protein is substituted by Ser. The OCIF of the invention has a
CC    molecular weight by SDS-PAGE of 60 kD under reducing conditions and
CC    120 kD under non-reducing conditions. The protein is adsorbed onto
CC    cation-exchangers or heparin and its activity is lowered after 10 mins
CC    at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
CC    deg.C. OCIF is useful in the control of bone resorption and therefore
CC    in the treatment and prevention of disorders of bone resorption, e.g.
CC    osteoporosis.
SQ    Sequence 1206 BP; 389 A; 283 C; 270 G; 264 T;
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Query Match 78.6%; Score 1200; DB 27; Length 1206;
Best Local Similarity 99.8%; Pred. No. 0.00e+00;
Matches 1203; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy    286 cacaaccgcgtgtgcgaatgcaagaaagggcgctaccttgagatagagtttctgcttgaa 360
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Db    301 cacaaccgcgtgtgcgaatgcaagaaagggcgctaccttgagatagagtttctgcttgaa 360

Qy    301 CACAACCGCGTGTGCGAATGCAAGAAAGGGCGCTACCTTGAGATAGAGTTTCTGCTTGAA 405
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    346 CACAACCGCGTGTGCGAATGCAAGAAAGGGCGCTACCTTGAGATAGAGTTTCTGCTTGAA 405

Qy    346 cataggagctgccctcctggaatttggaggtggtgcaaagctgggaaccccaagagaaatca 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 cataggagctgccctcctggaatttggaggtggtgcaaagctgggaaccccaagagaaatca 420

Qy    406 CATAGGAGCTGCCCTCCTGGAATTTGGAGGTGGTGCAAAGCTGGGAACCCCAAGAGAAATCA 465
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Db    406 CATAGGAGCTGCCCTCCTGGAATTTGGAGGTGGTGCAAAGCTGGGAACCCCAAGAGAAATCA 465

Qy    421 gtttgcaaagatgtccagatgggttcttctcctcaaaatgaagacgtcaatcaatcgt 480
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Db    466 GTTTGCAAAGATGTCCAGATGGTTCTTCTCCTCAAAATGAAGACGTCATCGAATCGT 525

Qy    466 gtttgcaaagatgtccagatggttcttctcctcaaaatgaagacgtcatcgaatcgt 525
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Db    481 agaaaacacacaacaaattgcagtgtcttttggtctccgaacctaaagttcaccaaca 540

Qy    481 agaaaacacacaacaaattgcagtgtcttttggtctccgaacctaaagttcaccaaca 540
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Db    526 AGAAAACACACAACAAATTGCAGTGTCTTTTGGTCTCCGAACCTAAAGTTCACCACA 585

Qy    526 AGAAAACACACAACAAATTGCAGTGTCTTTTGGTCTCCGAACCTAAAGTTCACCACA 585
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Db    541 cacggacacatatgttccggaaaacagtcaaaagtgagagagtgtagagagata 600

Qy    541 agtgtcttggtagacaaatttggctggtgcaccaaagtaaccgagagagtgtagagagata 600
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Db    586 cacggacacatatgttccggaaaacagtcaaaagtgagagagtgtagagagata 600

Qy    586 CACGGACACATATGTTCCGGAAAACAGTCAAAAGTGAGAGAGTGTAGAGAGATA 645
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Db    601 ctgtgtgaggaggcaattcttcagtttctgttcctacaaagtttaccgcctaactggctt 660

Qy    601 ctgtgtgaggaggcaattcttcagtttctgttcctacaaagtttaccgcctaactggctt 660
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Db    661 agtgtcttggtagacaaatttggctggtgcaccaaagtaaccgagagagtgtagagagata 720

Qy    661 agtgtcttggtagacaaatttggctggtgcaccaaagtaaccgagagagtgtagagagata 720
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Db    706 AGTGTCTTGGTAGACAAATTTGGCTGGTGCACCAAAGTAAACCGCAGAGAGTGTAGAGGATA 765

Qy    706 AGTGTCTTGGTAGACAAATTTGGCTGGTGCACCAAAGTAAACCGCAGAGAGTGTAGAGGATA 780
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Db    721 aaacggcaacacagctcacacaagaacagacttccagctgctggaagttatggaaacataa 780

Qy    721 aaacggcaacacagctcacacaagaacagacttccagctgctggaagttatggaaacataa 780
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Db    766 AAACGGCAACACAGCTCACAACAAGAACAGACTTTCCAGCTGCTGAAGTTATGGAAACATCAA 825

Qy    766 AAACGGCAACACAGCTCACAACAAGAACAGACTTTCCAGCTGCTGAAGTTATGGAAACATCAA 840
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Db    826 AACAAAGACCAAGATATAGTCAAGAAGAAGTCATCCAAGATATTGACCTCTGTGAAAACAGC 885

Qy    781 aacaaagaccaagatatagtcaagaagaagtcatccaagatattgacctctgtgaaaacagc 840
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Qy    826 AACAAAGACCAAGATATAGTCAAGAAGAAGTCATCCAAGATATTGACCTCTGTGAAAACAGC 885
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Db    886 GTGCAGCGGCACATTGGACATGCTAACCTCACCTTCGAGCTTTCGTAGCTTGATGGAA 945

Qy    841 gtgcagcggcacattggacatgctaacctcaccttcgagcttagcttgatggaa 900
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Qy    886 GTGCAGCGGCACATTGGACATGCTAACCTCACCTTCGAGCTTTCGTTGATGGAA 945
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Db    901 agcttaccgggaaagaaagtgggagcagaagacattgaaaaaacaataaaagcatgcaa 960

Qy    901 agcttaccgggaaagaaagtgggagcagaagacattgaaaaaacaataaaagcatgcaa 960
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Db    946 AGCTTACCGGGAAAGAAAGTGGGAGCAGAAGACATTGAAAAAACAATAAAAGCATGCAAA 1005

Qy    946 AGCTTACCGGGAAAGAAAGTGGGAGCAGAAGACATTGAAAAAACAATAAAAGCATGCAAA 1020
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Qy   1066 ACCTTGAAGGGCCTAATGCACGCACTAAAGCACTCAAAGACGTACCACTTTCCCAAAACT 1125

Db   1081 gtcactcagagtctaaagaagaccatcaggttccttcacagcttcacaatgtacaaattg 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1126 GTCACTCAGAGTCTAAAGAAGACCATCAGGTTCCTTCACAGCTTCACAATGTACAAATTG 1185

Db   1141 tatcagaagttattttagaaatgataggtaaccaggtccaatcagtaaaaataagctgc 1200
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Qy   1186 TATCAGAAGTTATTTTAGAAATGATAGGTAACCAGGTCCAATCAGTAAAAATAAGCTGC 1245

Db   1201 ttataa 1206
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Qy   1246 TTATAA 1251

RESULT    6
     T33163 standard; DNA; 1206 BP.
     T33163;
DT   22-APR-1997  (first entry)
DE   Mutated OCIF, OCIF-C21S, coding sequence.
KW   Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
KW   osteoporosis; ss.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   sig_peptide     1..63
FT   /*tag=  a
FT   mat_peptide     64..1203
FT   /*tag=  b
FT   /product= OCIF-C21S
PN   WO9626217-A1.
PD   29-AUG-1996.
PF   20-FEB-1996; J00374.
PR   20-FEB-1995; JP-054977.
PR   21-JUL-1995; JP-207508.
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
PI   Goto M,  Higashio K,  Kobayashi F,  Mochizuki S,  Morinaga T;
PI   Nakagawa N, Shima N,  Tsuda E,  Ueda M,  Yano K,  Yasuda H;
DR   WPI; 96-402320/40.
DR   P-PSDB; R99933.
PT   DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT   for bone resorption control, esp. treatment of osteoporosis
PS   Claim 33; Page 134-135; 183pp; Japanese.
CC   This sequence encodes a mutated version of the full length
CC   osteoclastogenesis inhibitory factor (OCIF) of the invention.  This
     sequence encodes OCIF-C21S in which the 21st Cys residue in the mature
     OCIF protein is substituted by Ser.  The OCIF of the invention has a
CC   molecular weight by SDS-PAGE of 60 kD under reducing conditions and
CC   120 kD under non-reducing conditions.  The protein is adsorbed onto
CC   cation-exchangers or heparin and its activity is lowered after 10 mins
CC   at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
CC   deg.C.  OCIF is useful in the control of bone resorption and therefore
CC   in the treatment and prevention of disorders of bone resorption, e.g.
CC   osteoporosis.
SQ   Sequence   1206 BP;    389 A;    286 C;    267 G;    264 T;

  Query Match             78.5%;  Score 1198;  DB 27;  Length 1206;
  Best Local Similarity  99.7%;  Pred. No. 0.00e+00;
  Matches  1202;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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Db     61 caggaaacgtttcctccaaagtaccttcattatgacgaagaaacctctcatcagctgttg 120
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Qy    106 CAGGAAACGTTTCCTCCAAAGTACCTTCATTATGACGAAGAAACCTCTCATCAGCTGTTG 165

Db    121 tgtgacaaatgtcctcctggtacctacctaaaacaacactgtacagcaaagtggaagacc 180
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Qy    166 TGTGACAAATGTCCTCCTGGTACCTACCTAAAACAACACTGTACAGCAAAGTGGAAGACC 225

Db    181 gtgtgcgccccttgccctgaccactactacacagacagctggcacaccactgacgagtgt 240
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Db    241 ctatactgcagccccgtgtgcaaggagctgcagtacgtcaagcaggagtgcaatcgcacc 300
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Qy    346 CACAACCGCGTGTGCGAATGCAAGGAAGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAA 405

Db    361 cataggagctgccctcctggatttggagtggtgcaagctggaaccccagagcgaaataca 420
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Qy    406 CATAGGAGCTGCCCTCCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGAAATACA 465

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Qy    526 AGAAAACACACAAATTGCAGTGTCTTTGGTCTCCTGCTAACTCAGAAAGGAAATGCAACA 585

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Db    601 ctgtgtgaggaggcattcttcaggtttgctgttcctacaaagtttacgcctaactggctt 660
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Qy    646 CTGTGTGAGGAGGCATTCTTCAGGTTTGCTGTTCCTACAAAGTTTACGCCTAACTGGCTT 705

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Qy    706 AGTGTCTTGGTAGACAATTTGCCTGGCACCAAAGTAAACGCAGAGAGTGTAGAGAGGATA 765

Db    721 aaacggcaacacagctcacaagaacagactttccagctgctgaagttatggaaacatcaa 780
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Qy    766 AAACGGCAACACAGCTCACAAGAACAGACTTTCCAGCTGCTGAAGTTATGGAAACATCAA 825

Db    781 aacaaagaccaagatatagtcaagaagatcatccaagatattgacctcagtgaaaacagc 840
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Qy    826 AACAAAGACCAAGATATAGTCAAGAAGATCATCCAAGATATTGACCTCTGTGAAAACAGC 885

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Qy    886 GTGCAGCGGCACATTGGACATGCTAACCTCACCTTCGAGCAGCTTCGTAGCTTGATGGAA 945

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Qy    946 AGCTTACCGGGAAAGAAAGTGGGAGCAGAAGACATTGAAAAAACAATAAAGGCATGCAAA 1005

Db    961 cccagtgaccagatcctgaagctgctcagtttgtggcgaataaaaaatggcgaccaagac 1020
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Qy   1006 CCCAGTGACCAGATCCTGAAGCTGCTCAGTTTGTGGCGAATAAAAAATGGCGACCAAGAC 1065

Db   1021 accttgaagggcctaatgcacgcactaaagcactcaaagacgtaccactttcccaaaact 1080
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Qy   1066 ACCTTGAAGGGCCTAATGCACGCACTAAAGCACTCAAAGACGTACCACTTTCCCAAAACT 1125

Db   1081 gtcactcagagtctaaagaagaccatcaggttccttcacaccttcacaatgtacaaattg 1140
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Qy   1126 GTCACTCAGAGTCTAAAGAAGACCATCAGGTTCCTTCACAGCTTCACAATGTACAAATTG 1185

Db   1141 tatcagaagttattttagaaatgataggtaaccaggtccaatcagtaaaaataagctgc 1200
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Qy   1246 TTATAA 1251
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RESULT 7

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ID   T33172 standard; DNA; 1200 BP.
AC   T33172;
DT   22-APR-1997  (first entry)
DE   Mutated OCIF, OCIF-CL, coding sequence.
KW   Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
KW   osteoporosis; ss.
OS   Synthetic.
FH   Key              Location/Qualifiers
FT   sig_peptide      1..63
FT                    /*tag= a
FT   mat_peptide      64..1197
FT                    /*tag= b
FT                    /product= OCIF-CL
PN   WO9626217-A1.
PD   29-AUG-1996.
PF   20-FEB-1996; J00374.
PR   20-FEB-1995; JP-054977.
PR   21-JUL-1995; JP-207508.
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
PI   Goto M, Higashio K, Kobayashi F, Mochizuki S, Moriaga T;
PI   Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
DR   WPI; 96-402320/40.
DR   P-PSDB; R99942.
PT   DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT   for bone resorption control, esp. treatment of osteoporosis
PS   Claim 60; Page 143-144; 183pp; Japanese.
CC   This sequence encodes a mutated version of the full length
CC   osteoclastogenesis inhibitory factor (OCIF) of the invention. This
CC   sequence encodes OCIF-CL in which amino acids 379-380 of the mature
CC   protein have been deleted. The OCIF of the invention has a molecular
CC   weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under
CC   non-reducing conditions. The protein is adsorbed onto cation-exchangers
CC   or heparin and its activity is lowered after 10 mins at 90 deg.C or 30
CC   mins at 56 deg.C, and is lost after 10 mins at 70 deg.C. OCIF is useful
CC   in the control of bone resorption and therefore in the treatment and
CC   prevention of disorders of bone resorption, e.g. osteoporosis.
SQ   Sequence 1200 BP; 387 A; 283 C; 268 G; 262 T;

Query Match          78.38;  Score 1196;  DB 27;  Length 1200;
Best Local Similarity 99.8%;
Matches 1197; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Pred. No. 0.00e+00;
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Db      1 atgaacaacttgctgtcgctgcgcgcgcgtctctggacatctccattaagtggaccacc   60
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Qy    106 CAGGAAACGTTTCCTCCCAAAGTAACCTTCATTATGACGAAGAAAACCTCTCATCAGCTGTTG 165

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Qy    166 TGTGACAAATGTCCTCCTGTTACCTTAAAAACAACACTGTACGCAAAGTGGAAGACC       225

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Db    301 cacaaccgcgtgtgcgaatccaagggaaggaagggcgctacctta                   360
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Qy    406 CATAGGAGCTGCCCTCCTGGATTTGGAGTGGTGCAAGCTGGAACCCAGAGACGAAATACA   465

Db    421 gtttgcaaagatgtccagtgtggttcttcaaatgagacgcatcatctaaagcaccctgt     480
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Qy    466 GTTTGCAAAGATGTCCAGATGTGGTTCTTCTCAAATGAGACGTCATCATCTAAAGCACCCTGT 525

Db    481 agaaaacacacaaaattgcagtgtgtctttggttctcctcctccagaaagaaagtgcaaca   540
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Qy    586 CACGACAACATATGTTCCGGAAACAGTGAATCAACTCAAAAAAATGTGGAATAGATGTTACC  645

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Qy    646 CTGTGTGAGAGGCATTCCAGGTTTTGTGTTCCTACAAAGTTTACGCCTAACTGGCTT      705

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Qy    706 AGTGTCTTGGTAGACAAATTTGCCCTGGCCACCAAAGTAAACGACGAGAGGTCGGAGGATA  765

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Qy    766 AAAACGGCAACACAGCTCAACAAGAAACAGACTTTCCAGCTGCTGCTGAAGTTATGGAAACATCAA 825

Db    781 aacaaagaccaagatatagtcaagaagaatcatccagagatattgacctctgtgaaaacagc  840
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Qy    826 AACAAAGACCAAGATATAGTCAAGAAGAATCATCCAGAGATATTGACCTCTGTGAAAACAGC  885

Db    841 gtgcaggcgcacattggacatgctaacctcaccttgagcagcttgtagttgatggaa     900
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Qy    886 GTGCAGCGGCGCACATTGGACATGCTAACCTCACCTTGAGCAGCTTGTAGTTGATGGAA     945

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Qy    946 AGCTTACCGGGAAAGAAAGTGGGAGCAGAAGACATTGAAAAAACAATAAAGCCATGCAAA  1005

Db    961 cccagtgaccagatcctgaagtgctcagttctgtgggaattaaaaatggcgaccaagac  1020
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Qy   1006 CCCAGTGACCAGATCCTGAAGTGCTCCAGTTTGTGTGGGCGAATTAAAAAATGGCGACCAAGAC 1065

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Qy   1066 ACCTTGAAGGGCGGCCTAAGTGCAGGCACACTCAAAGAGACTTACCACTTTCCCAAAAACT 1125

Db   1081 gtcaactcagagtctaaagaagaccatcagttccttcacagctcacaagtagctacaaattg 1140
          |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Qy   1126 GTCACTCAGATGTCTAAAAGAAGAACCATCAGGTTCCTTCACAGCTTCACAAGTAGCTACAAATTG 1185

Db   1141 tatcagaagttatttttagaaaataacaggtaacaacaataaagtaaaaataagct        1198
          ||||||||||||||||||| ||| ||| |||| ||||||||| ||||| |||||||
Qy   1186 TATCAGAAGTTATTTTTAGAAAATGATAGGTAACAACCAGTCCAATCAGTAAAAATAAGCT 1243
```

RESULT 8

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ID   T33178 standard; DNA; 1182 BP.
AC   T33178;
DT   22-APR-1997  (first entry)
DE   Mutated OCIF, OCIF-CBst, coding sequence.
KW   Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
KW   osteoporosis; ss.
OS   Synthetic.
FH   Key              Location/Qualifiers
FT   sig_peptide      1..63
FT                    /*tag= a
FT   mat_peptide      64..1179
FT                    /*tag= b
FT                    /product= OCIF-CBst
PN   WO9626217-A1.
PD   29-AUG-1996.
PF   20-FEB-1996; J00374.
PR   20-FEB-1995; JP-054977.
PR   21-JUL-1995; JP-207508.
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
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PI   Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
PI   Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
DR   WPI; 96-402320/40.
RP   P-PSDB; R99948.
PT   DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT   for bone resorption control, esp. treatment of osteoporosis
PS   Claim 78; Page 148; 183pp; Japanese.
CC   This sequence encodes a mutated version of the full length
CC   osteoclastogenesis inhibitory factor (OCIF) of the invention. This
CC   sequence encodes OCIF-CBst in which Gln371 is substituted with Leu
CC   and amino acids 373-380 of the mature protein have been deleted. These
CC   amino acid changes have been caused by the introduction of a restriction
CC   site. The OCIF of the invention has a molecular weight by SDS-PAGE of
CC   60 kD under reducing conditions and 120 kD under non-reducing
CC   conditions. The protein is adsorbed onto cation-exchangers or heparin
CC   and its activity is lowered after 10 mins at 70 deg.C or 30 mins at 56
CC   deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful in the
CC   control of bone resorption and therefore in the treatment and
CC   prevention of disorders of bone resorption, e.g. osteoporosis.
SQ   Sequence 1182 BP; 376 A; 280 C; 266 G; 260 T;
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```
Query Match             76.8%;  Score 1173;  DB 27;  Length 1182;
Best Local Similarity   99.7%;
Matches 1176;  Conservative 0;  Mismatches 3;  Indels 0;  Gaps 0;
Pred. No. 0.00e+00;

Qy    1  atgaacaacttgtctgtgtgcgcgctcgtgttctggacatctccattaagtgaccacc   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   46  ATGAACAACTTGTCTGTGTGCGCGCTCGTGTTCTGGACATCTCCATTAAGTGACCACC  105

Qy   61  caggaaacgtttcctccaaagtaccttcaattatgacgaagaaaacctctcactgctgttg  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  106  CAGGAAACGTTTCCTCCAAAGTACCTTCAATTATGACGAAGAAAACCTCTCACTGCTGTTG  165

Qy  121  tgtgacaaaatgtcctcctggtactactaccgtaaaacaacagctgtacagcaaaagtggaagacc  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  166  TGTGACAAAATGTCCTCCTGGTACTACTACCGTAAAACAACAGCTGTACAGCAAAAGTGGAAGACC  225

Qy  181  gtgtgcgccccttgcccctgaccactacacacagacagcgtggcacaccagtgacgagtgt  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  226  GTGTGCGCCCCTTGCCCCTGACCACTACACACAGACAGCGTGGCACACCAGTGACGAGTGT  285

Qy  241  ctatactgcagccccgtgtgcaagaagagctccagtacgtcaagcacaaatcgcacc  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  286  CTATACTGCAGCCCCGTGTGCAAGAAGAGCTCCAGTACGTCAAGCACAAATCGCACC  345

Qy  301  cacaaccgcgtgtgcgaatcaaggaagggcgcgctaccttgagatagagttctgcttgaaa  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  346  CACAACCGCGTGTGCGAATCAAGGAAGGGCGCGCTACCTTGAGATAGAGTTCTGCTTGAAA  405

Qy  361  cataggagctgcctccctggatttggacgtgcaagctggaaccccagagcgaaataca  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  406  CATAGGAGCTGCCTCCCTGGATTTGGACGTGCAAGCTGGAACCCCAGAGCGAAATACA  465

Qy  421  gtttgcaaagatgtccaggttgttctttctcaaatgagagctcatctaaagcaccctgt  480
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  466  GTTTGCAAAGATGTCCAGGTTGTTCTTTCTCAAATGAGAGCTCATCTAAAGCACCCTGT  525

Qy  481  agaaaacacacaaaattgcagtgtctttggttcttctctcctgctaactcagaaaatgcaaca  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  526  AGAAAACACACAAAATTGCAGTGTCTTTGGTTCTTCTCTCCTGCTAACTCAGAAAATGCAACA  585

Qy  541  cacgacacatatgttccggaaacagtgaatcaactcaaaaatgtggaatagatgttacc  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  586  CACGACACATATGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACC  645

Qy  601  ctgtgtgaggaggaccattccacggcattcacgttgcttacacaaagtttacggctaactggctt  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  646  CTGTGTGAGGAGGACCATTCCACGGCATTCACGTTGCTTACACAAAGTTTACGGCTAACTGGCTT  705

Qy  661  agtgtcttcggtagacaaattgcctggcaccaaagtaaaggcagagagtgtagagaggata  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  706  AGTGTCTTCGGTAGACAAATTGCCTGGCACCAAAGTAAAGGCAGAGAGTGTAGAGAGGATA  765
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RESULT 9
ID   T33173 standard; DNA; 1056 BP.
AC   T33173;
DT   22-APR-1997 (first entry)
DE   Mutated OCIF, OCIF-CC, coding sequence.
KW   Osteoclastogenesis inhibitory factor; OCIF-CC.
KW   Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
KW   osteoporosis; ss.
OS   Synthetic.
FH   Key             Location/Qualifiers
FT   sig_peptide     1..63
FT   /*tag= a
FT   mat_peptide     64..1053
FT   /*tag= b
FT   /product= OCIF-CC
PN   WO9626217-A1.
PD   29-AUG-1996.
PF   20-FEB-1996; JP-054977.
PR   20-FEB-1995; JP-054977.
PR   21-JUL-1995; JP-207508.
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
PI   Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
PI   Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
DR   WPI; 96-402320/40.
RP   P-PSDB; R99943.
PT   DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT   for bone resorption control, esp. treatment of osteoporosis
PS   Claim 63; Page 144-145; 183pp; Japanese.
CC   This sequence encodes a mutated version of the full length
CC   osteoclastogenesis inhibitory factor (OCIF) of the invention. This
CC   sequence encodes OCIF-CC in which amino acids 331-380 of the mature
CC   protein have been deleted. The OCIF of the invention has a molecular
CC   weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under
CC   non-reducing conditions. The protein is adsorbed onto cation-exchangers
CC   or heparin and its activity is lowered after 10 mins at 70 deg.C or 30
CC   mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful
CC   in the control of bone resorption and therefore in the treatment and
CC   prevention of disorders of bone resorption, e.g. osteoporosis.
SQ   Sequence 1056 BP; 332 A; 252 C; 247 G; 225 T;
```

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Query Match             68.9%;  Score 1052;  DB 27;  Length 1056;

Qy  766  aaacggcaacagctcacaagaacagagactttccagctcgtgctgaaggttatggaaacatcaa  825
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  721  AAACGGCAACAGCTCACAAGAACAGAGACTTTCCAGCTCGTGCTGAAGGTTATGGAAACATCAA  780

Qy  826  gtgtgcggcggccaattgtcatgctaacctcaacctccatgctaataacgaagatgctaacc  885
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  781  GTGTGCGGCGGCCAATTGTCATGCTAACCTCAACCTCCATGCTAATAACGAAGATGCTAACC  840

Qy  886  gtgcaggcggcacattggacatgctaacctcaacctcgagcgtcgtgatggaa  945
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  841  GTGCAGGCGGCACATTGGACATGCTAACCTCAACCTCGAGCGTCGTGATGGAA  900

Qy  946  agcttacccgggaagaagaagtgggagcagaagacaaatatgaaaaaaacaataaagcaa  1005
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  901  AGCTTACCCGGGAAGAAGAAGTGGGAGCAGAAGACAAATATGAAAAAAACAATAAAGCAA  960

Qy 1006  cccagtgaccagatccctgaagctgtcctcagtttgttggcgcgaataggcgaccaagac  1065
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  961  CCCAGTGACCAGATCCCTGAAGCTGTCCTCAGTTTGTTGGCGCGAATAGGCGACCAAGAC 1020

Qy 1066  accttgaaggggcctaatgcacgcactcaaagcacactgtaccactttcccaaaaact  1125
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1021  ACCTTGAAGGGGCCTAATGCACGCACTCAAAGCACACTGTACCACTTTCCCAAAAACT 1080

Qy 1126  gtcactcagagtctaaagaagaacatcaggttccttcacagcttcacaagtacaaattg  1185
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1081  GTCACTCAGAGTCTAAAGAAGAACATCAGGTTCCTTCACAGCTTCACAAGTACAAATTG 1140

Qy 1185  tatcagaagttattttttagaaaatgattaggtaacctagtc  1224
         |||||||||||||||||||||||||||||||||||||||||
Db 1141  TATCAGAAGTTATTTTTTAGAAAATGATTAGGTAACCAGGTC 1179
```

First alignment block

Best Local Similarity 99.9%; Pred. No. 0 0.00e+00;
Matches 1053; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db     1 atgaacaacttgtctgtgtcgcgcctgtgtttctggacatctccattaagtgaccacc   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    46 ATGAACAACTTGCTGTGTCGCGCCTGTGTTTCTGGACATCTCCATTAAGTGACCACC  105

Db    61 caggaaacgttctcccaagtacctcattatgacgaggaaacctctcatcagctgttg  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   106 CAGGAAACGTTTCCTCCAAAGTACCTCATTATGACGAGGAAACCTCTCATCAGCTGTTG  165

Db   121 tgtgacaaatgtctcctcctggtacctcacagacaacactgtacagaagtggaagacc  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   166 TGTGACAAATGTCCTCCTCCTGGTACCTCACAGACAACACTGTACAGAAGTGGAAGACC  225

Db   181 gtgtgcgcccctctgccctcgaccactactcacacaacacagtggcaccagtgacgagtgt  240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   226 GTGTGCGCCCCTTGCCCTCGACCACTACTCACACAACAACACAGTGGCACCAGTGACGAGTGT  285

Db   241 ctatactgcagcccgtgctgcaaggaaggagagctgcaagtacgtcaagcaggagtcaac  300
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   286 CTATACTGCAGCCCGTGCTGCAAGGAAGGAGAGCTGCAAGTACGTCAAGCAGGAGTCAAC  345

Db   301 cacaaccggtgtgtggaatgcaaggaaggcgctacctgaggatagagttctgcttgaaa  360
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   346 CACAACCGGTGTGTGGGAAATGCAAAGGAAGGCGCTACCTTGAGGATAGAGTTCTGCTTGAAA  405

Db   361 cataggagagctgccctcctgatttggagtgttgcaagctggaacccgaagcgcgaaataca  420
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   406 CATAGGAGCTGCCCTCCTGATTTGGAGTGGTGCAAGCTGGAACCCGAGACGGCGAAATACA  465

Db   421 gtttgcaaagagatgtccaagatgtgggttcttctctccaaatgagacgtcatctcaaagcaccctgt  480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   466 GTTTGCAAAAGAGATGTCCAAGATGGGTTCTTCTCTCCAAATGAGACGTCATCTAAAAGCACCCCTGT  525

Db   481 agaaaacacacacaaattgcagtgtctttggtctcctgctaactcagaaatgaaatgcaaca  540
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   526 AGAAAACACACAAAATTGCAGTGTCTTTGGTCTCCTACTCAGAAAAGAAAATGCAACA  585

Db   541 cacgacaacatatgttccggaaacagtgaatcaactcaaaaatgtggaatagatgttacc  600
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   586 CACGACAACATATGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACC  645

Db   601 ctgtgtgaggaggcattcttcaaggttttgctgttcctacaaagtttacgcctaactggctt  660
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   646 CTGTGTGAGGAGGCAATTCTTCAGGTTTGCTGTTTCCTACAAAGTTTACGCCTAACTGGCTT  705

Db   661 agtgtcttgtagacaatttgcctggcacaagtaaacccagagagtgtagagaggata  720
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   706 AGTGTCTTGTTGTAGACAAATTTGCCTGGCACACAAGTAAAACCCAGAGAGTGTAGAGAGGATA  765

Db   721 aaacggcaacacagctcacaagaacaagacttttccagctgtctgaagttatggaaacatcaa  780
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   766 AAACCGGCACACAGCTCACAAGAACAAGACTTTCCAGCTGTCTGAAGTTATGGAAACATCAA  825

Db   781 aacaaagaccaagatatagtcaaagaagatcatccaaagtagacctctgtgaaaacagc  840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   826 AACAAAGACCAAGATATAGTCAAAGAAGATCATCCAAAGATARTTGACCTCTGTGAAAACAGC  885

Db   841 gttgcagcggcacattggacatgctaacctcacctcgagcagcttcgttagcttgatggaa  900
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   886 GTTGCAGCGGCACATTGGGACATGCTAACCTCACCTTCGGTACCTTGACTTGGATGGAA  945

Db   901 agcttaccggaaagaaagtggaagcagaagacattgaaaaaacaataaaggcatgcaa  960
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   946 AGCTTACCCGGAAAGAAAGTGGGACGAAGACATTGAAAAAACAATAAAAGGCATGCAAA  1005

Db   961 cccagtgaccagatccctgaagctgtctcaagactgcttcagttcagcctgatcgaaac  1020
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  1006 CCCAGTGACCAGATCCTGAAGCTGTCTCAGTTTGTGGCGAATAAAAAATGGGACCAAGAC  1065

Db  1021 accttgaaaggccctaatgcacgcacctaaagcact  1054
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Second alignment block

Query Match 66.6%; Score 1017; DB 27; Length 1083;
Best Local Similarity 100.0%; Pred. No. 0 0.00e+00;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1066 ACCTTGAAAGGGCCTAATGCACGCACTAAAGCACT  1099

Db      67 ccttgccctgaccactactaacacagcagcgtgacaacagtgtgacaagtgtctatactgc  126
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     235 CCTTGCCCTGACCACTACTACACACAGACAACAGTGACGAGTGTCTATACTGC  294

Db     127 agcccgtgtgcaaggagagctgcagtacgtcaagcaggaggtgcaatcgcaccacaacgc  186
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     295 AGCCCGTGTGCAAGGAGAGCTGCAGTACGTCAAGCAGGAGGTGCAATCGCACCACAACCGC  354

Db     187 gtgtgcggaatgcaaggaaggcgctaccttgagaatagagttctgcttgaaaacataggagc  246
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     355 GTGTGCGGAATGCAAAGGAAGGGCCTACCTTGAGGATAGAGTTCTGCTTGAAAACATAGGAGC  414

Db     247 tgccctcctgatttggagtggtgcaagctggaaccccagagcgcgaaatacagtttgcaa  306
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     415 TGCCCTCCTGGATTTGGAGTGGTGCAAGCTGGAACCCCAGAGCGGAAATACAGTTTGCAAA  474

Db     307 agatgtccagtggggttctttctcaaatgagagtcatctaaagcaccctgaaaacac  366
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     475 AGATGTCCAGATGGGGTTCTTTCTCAAATGAGAGCGTCATCTAAAGCACCCTGRAGAAAACAC  534

Db     367 acaaattgcagtgtctttggttcttctcctgctaacttcagaaaagaaaatgcaacacgacaac  426
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     535 ACAAATTGCAGTGTCTTTGGTCTTTGGTCTCCTGCTAACTCAGAAAAGAAAATGCAACACGACAAC  594

Db     427 atatgttccggaaacagtgaatcaactcaaaaatgtggaatagatgttacccctgtgtgtgag  486
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     595 ATATGTTCCGGAAACAGTGAATCAACTCAAAAATGTGGAATAGATGTTACCCTGTGTGTGAG  654
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RESULT 11

ID   T33179 standard; DNA; 966 BP.
AC   T33179;
DT   22-APR-1997  (first entry)
DE   Mutated OCIF, OCIF-CSph, coding sequence.
KW   Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
KW   osteoporosis; ss.
SQ   Sequence 966 BP; 301 A; 228 C; 226 G; 211 T;

FH   Key             Location/Qualifiers
FH
FT   sig_peptide     1..63
FT   /*tag=  a
FT   mat_peptide     64..963
FT   /*tag=  b
FT   /product=  OCIF-CSph
FT
PN   WO9626217-A1.
PD   29-AUG-1996.
PF   20-FEB-1996; J00374.
PR   20-FEB-1995; JP-054977.
PR   21-JUL-1995; JP-207508.
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
PI   Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
PI   Nakagwa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
DR   WPI; 96-40320/40.
DR   P-PSDB; R99949.
PT   DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT   for bone resorption control, esp. treatment of osteoporosis
PS   Claim 81; Page 149; 183pp; Japanese.
CC   This sequence encodes a mutated version of the full length
CC   osteoclastogenesis inhibitory factor (OCIF) of the invention. This
CC   sequence encodes OCIF-CSph in which amino acids 298-380 of the mature
CC   protein have been deleted and replaced by Ser-Leu-Asp. These amino
CC   acid changes have been caused by the introduction of a restriction
CC   site. The OCIF of the invention has a molecular weight by SDS-PAGE of
CC   60 kD under reducing conditions and 120 kD under non-reducing
CC   conditions. The protein is adsorbed onto cation-exchangers or heparin
CC   and its activity is lowered after 10 mins at 90 deg.C. OCIF is useful in the
CC   deg.C, and is lost after 10 mins at 70 deg.C or 30 mins at 56
CC   control of bone resorption and therefore in the treatment and
CC   prevention of disorders of bone resorption, e.g. osteoporosis.

Query Match      62.3%;  Score 951;  DB 27;  Length 966;
Best Local Similarity  99.9%;  Pred. No. 0.00e+00;
Matches  952;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;
```

DNA sequence alignment (Qy = query, Db = database; flanking numbers are residue positions):

```
Qy       1  atgaacaacttgctgtgtgtcgggctcgtcgttcctggttctggacatctccattaagtggaccacc      60
Db      46  ATGAACAACAGTTGCGTGCTGCGGGCTCCGTGTTCTCCATTAAGTGGACCACC     105

Qy      61  cagggaaacgttttcctccaaagtacctcattatgacgaaagaacctctcatcagctgttg     120
Db     106  CAGGAAACGTTTTCCTCCAAAGTACCTTCATTATGACGAAAGAAACCTCTCATCAGCTGTTG    165

Qy     121  tgtgacaaatgtcctcctggttacctcactccta...aaaacctaaaagtcgaagacc     180
Db     166  TGTGACAAATGTCCTCCTGGTTACCTCACTCCTAAAAAACAACAACACTGTACAGCAAAGTGGAAGACC    225

Qy     181  gtgtgcggcgcccctgcgcccctgtgtcaaggagctgcaagagc...gacgagtgt     240
Db     226  GTGTGCGGCGCCCCTTGCGCCCTGTGTCAAGGAGCTGCAAGAGCACACAGTGCACCAGCGTGT    285

Qy     241  ctatactgcagccccgtgtgcaaggagctgcagtgagtcaatcgcacc     300
Db     286  CTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTAGCGTACGTCAAGCGAATCGCACC    345

Qy     301  cacaaccgcgttgtgcgaatgcaaggagaagggcgctaccttgagataggagttcgcttgaaa     360
Db     346  CACAACCGCGTGTGCGAATGCAAGGAAGAGGGCGCTACCTTGAGATAGGAGTTCGCTTGAAA     405

Qy     361  cataggaagctgcccctcctggatttgggagtggttgcaagccaagccccagagagaaata     420
Db     406  CATAGGAAGCTGCCCCTCCTGGATTTGGGACGGTCGCAAGCTGGAACCCCAGAGCGGAAAATACA    465

Qy     421  gtttgcaaaagtgtcaagatgggttcttcctcaaatgagacgtcaatctaaagcaccctgt     480
Db     466  GTTTGCAAAAGAGATGTCAGATGGGTTCTTCTCTCAAATGAGACGTCATCTAAAGCACCCTGT    525

Qy     481  agaaaacacacacaaaattgcaagtgtcttttggtctcccgtcaactgcaaca     540
Db     526  AGAAAACACACAAAATTGCAGTGTCTTTTGGTCTCCCTGCTAACTCAACTGCCTT    585

Qy     541  cacgacacaacatatgttccggaacagtgaactcaaactcaaaaatgtggaatagtgttacc     600
Db     586  CACGACAACATATGTTCCGGAAACACAGTGAATCAACTCAAAAAATGTGGAATAGAAGTTACC    645

Qy     601  ctgtgtaggaggcattcctcaagttttgctgttcctacaactggctt     660
Db     646  CTGTGTGAGGAGGCATTCTTCAGGTTGCGTTTGCTGTTCCTACAACTGGCTT    705

Qy     661  agtgtcttggttagacaatttgcctggccaccaaagtaaacgcagagagtctaagagagata     720
Db     706  AGTGTCTTGGTAGACAATTTGCCTGGCCACCAAAGTAAACGCAGAGAGTCTAGAGAGGATA    765

Qy     721  aaacggcaacacagctcacaagacagacttccagtctgcttgaagtctagaaacctaa     780
Db     766  AAACGGCAACACAGCTCACAAGAACAGACTTCCAGTCTGCTTGAAGTATAGGAAACATCAA    825

Qy     781  aacaaagaccaagatagtcaagaagatcatccaagatattgacctctgtgaaaacagc     840
Db     826  AACAAAGACCAAGATATAGTCAAGAAGATCATCCAAGATATTGACCCTGTGAAAACAGC    885

Qy     841  gtgcagcaggcacattgaacatgctaacctcaacttcgagcagctagcttgatggaa     900
Db     886  GTGCAGCGCGCACATTGGACAATGCTAACCTCAACTTCGAGCAGCAGCTTGATGGAA     945
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Db     487  gaggcattcttcaggtttgctgtgttcctacaaagtttacgcctactggtgtcttg     546
Qy     655  GAGGCATTCTTCAGGTTTGCTGTTCCTACAACAAGTTTACGCCTACTGGTGTCTTG     714

Db     547  gtagacaatttgcctggccaccaaagtaaacgcagagagtagtagaggataaaacggcaa     606
Qy     715  GTAGACAATTTGCCTGGCCACCAAAGTAAACGCAGAGAGTGTAGAGAGGATAAAACGGCAA     774

Db     607  cacagctcacaagacagacttccagtctgcttgaagtctagaaaacatcaaaacaaagac     666
Qy     775  CACAGCTCACAAGAACAGACTTTCCAGTCTGCTTGAAGTTATGGAAACATCAAAACAAAGAC     834

Db     667  caagatatagtcaagaagatcatccaagatattgacctctgtgaaaacagcgtgcacgg     726
Qy     835  CAAGATATAGTCAAGAAGATCATCCAAGATATTGACCTCTGTGAAAAACAGCGTGCACGG     894

Db     727  cacattggacatgctaacctcaacttcgagcagctagcttgatggaaacagccagg     786
Qy     895  CACATTGGACATGCTAACCTCAACTTCGAGCAGCTTGATGGAAACAGCCAGG     954

Db     787  ggaaagaaagtggggagcagaaacacatgaaaaaaacaataaaaggcagtgatgac     846
Qy     955  GGAAAGAAAGTGGGGAGCAGAAACAATTGAAAAAAACAGCATTGAAAGGCAGTGATGAC    1014

Db     847  cagatcctgaagctgtcctcagtttgttgtggcggaataaaaatgggacc     906
Qy    1015  CAGATCCTGAAGCTGTCTCAGTTTGTTGTGGCGGAATAAAAATGGGACC    1074

Db     907  ggcctaatgcacgcactcaaagacgactgcaccttgaag     966
Qy    1075  GGCCTAATGCACGCACTAAAGACGACTGCACCTTGAAG    1134

Db     967  agtctaaagaagacatcaagttcctcaaatgtatcagaag    1026
Qy    1135  AGTCTAAAGAAGACCATCAAGTTCCTCAAATTGTATCAGAAG    1194

Db    1027  ttatttttagaaatgataggttaaccaggtccaatcagtaaaaataagctgcttata    1083
Qy    1195  TTATTTTTAGAAATGATAGGTTAACCAGGTCCAATCAGTAAAAATAAGCTGCTTATAA    1251
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RESULT 12
ID   T33167 standard; DNA; 1080 BP.
AC   T33167;
DT   22-APR-1997 (first entry)
DE   Mutated OCIF, OCIF-DCR2, coding sequence.
KW   Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
OS   Synthetic.
FH   Key            Location/Qualifiers
FT   sig_peptide    1..63
FT   /*tag= a
FT   mat_peptide    64..1077
FT   /*tag= b
FT   /product= OCIF-DCR2
PN   WO9626217-A1.
PD   29-AUG-1996;
PF   20-FEB-1996; J00374.
PR   20-FEB-1995; JP-054977.
PR   21-JUL-1995; JP-207508.
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
PI   Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
PI   Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
PS   Claim 45; Page 138-139; 183pp; Japanese.
PT   DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT   for bone resorption control, esp. treatment of osteoporosis
DR   WPI; 96-402320/40.
DR   P-PSDB; R99937.
CC   This sequence encodes a mutated version of the full length
CC   osteoclastogenesis inhibitory factor (OCIF) of the invention. This
CC   sequence encodes OCIF-DCR2 in which amino acids 43-84 of the mature
CC   protein have been deleted. The OCIF of the invention has a molecular
CC   weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under
CC   non-reducing conditions. The protein is adsorbed onto cation-exchangers
CC   or heparin and its activity is lowered after 10 mins at 70 deg.C or 30
CC   mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful
CC   in the control of bone resorption and therefore in the treatment and
CC   prevention of disorders of bone resorption, e.g. osteoporosis.
SQ   Sequence 1080 BP; 357 A; 243 C; 236 G; 244 T;

Query Match    58.38%;   Score 890;   DB 27;   Length 1080;
Best Local Similarity  99.9%;   Pred. No. 0.00e+00;
Matches  891;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy   189 cgaatgcaaggaaggcggcctacccttgagatagaagttctgtgcttgaaacataggagctgccc 248
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   360 CGAATGCAAGGAAGGGCGGCCTACCCTTGAGATAGAAGTTCTGCTTGAAACATAGGAGCTGCCC 419

Qy   249 tcctggattggagtggtgcaagctcggaacccagacgaaatacagtttgaaaagatg 308
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   420 TCCTGGATTGGAGTGGTGCAAGCTCGGAACCCAGACGAAATACAGTTTGAAAAGATG 479

Qy   309 tccagaatgggtgttcctccaaatgagacgtcatctaaagcacccgttagaaaacacacaa 368
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   480 TCCAGAATGGGTGTTCCTCTCAAATGAGACGTCATCTAAAGCACCCGTTAGAAAACACACAA 539

Qy   369 ttgcagtgtcttggtcctcctgctaactcagaaaggaaatccaacacacgacaacatatg 428
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   540 TTGCAGTGTCTTTTGGTCCTCCTGCTAACTCAGAAAGGAAATCCAACACACGACAACATATG 599

Qy   429 ttccggaaacgtgaatcaactcaaaaatgtggaataagtaccctgtgtgaggaggc 488
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   600 TTCCGGAAACGTGAATCAACTCAAAAATGTGGAATAAGTACCCTGTGTGAGGAGGC 659

Qy   489 atttctcaagtttgctgttcctccacaaagtttacgctaactggcttagtgtcttggtaga 548
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   660 AATTCTTCAAGTTTGCTGTTCCTCCACAAAGTTTACGGCTAACTGGTTAGTGTCTTGGTAGA 719

Qy   901 agcttaccggaaagaaagtggagacgaagagacattgaaaaaacaattaaagc 953
         ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   946 AGCTTACCGGAAAGAAAGTGGGAGACGAAGAGACATTGAAAAAACAATTAAAGGC 998
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RESULT 13
ID   T33171 standard; DNA; 984 BP.
AC   T33171;
DT   22-APR-1997 (first entry)
DE   Mutated OCIF, OCIF-DDD2, coding sequence.
KW   Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
OS   Synthetic.
FH   Key            Location/Qualifiers
FT   sig_peptide    1..63
FT   /*tag= a
FT   mat_peptide    64..981
FT   /*tag= b
FT   /product= OCIF-DDD2
PN   WO9626217-A1.
PD   29-AUG-1996;
PF   20-FEB-1996; J00374.
PR   20-FEB-1995; JP-054977.
PR   21-JUL-1995; JP-207508.
PA   (SNOW ) SNOW BRAND MILK PROD CO LTD.
PI   Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
PI   Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
PS   Claim 57; Page 142-143; 183pp; Japanese.
PT   DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT   for bone resorption control, esp. treatment of osteoporosis
DR   WPI; 96-402320/40.
DR   P-PSDB; R99941.
CC   This sequence encodes a mutated version of the full length
CC   osteoclastogenesis inhibitory factor (OCIF) of the invention. This
CC   sequence encodes OCIF-DDD2 in which amino acids 253-326 of the mature
CC   protein have been deleted. The OCIF of the invention has a molecular
CC   weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under
CC   non-reducing conditions. The protein is adsorbed onto cation-exchangers
CC   or heparin and its activity is lowered after 10 mins at 70 deg.C or 30
CC   mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is useful
CC   in the control of bone resorption and therefore in the treatment and

Qy   549 caatttgcctgccacccaagtaaagccagagagtgtagagatgagaggaggatcaaacggcaacacag 608
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   720 CAATTTGCCTGGCCACCCAAGTAAACGCCAGAGAGTGTAGAGATGAGAGGAGGATCAAACGGCAACACAG 779

Qy   609 ctcacaagaacagacttccagctgtctgaaagttatgtgaagttattgaaagcaatcaaaacaaagaa 668
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   780 CTCACAAGAACAGACTTCCAGCTGTCTGAAAGTTATGTGAAGTTATTGGAAAGCAATCAAAACAAAGAA 839

Qy   669 tatagtcaagaagatcatcccaagatattgacctctgaaagcacatt 728
         |||||||||||||||||||||||||||||||||||||||||||||||
Db   840 TATAGTCAAGAAGATCATCCCAAGATATTGACCTCTGAAAGCACATT 899

Qy   729 tggacaatgctaacctcaccttcgagcagcttcgtagtcttgatgaagttaccggggaa 788
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Db   900 TGGACAATGCTAACCTCACCTTCGAGCAGCTTCGTAGTCTTGATGAAGTTACCGGGAAA 959

Qy   789 gaaagtgggagcagaagaacattgaaaaaacaattaaagcagtcaaaccagtgagagat 848
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   960 GAAAGTGGGAGCAGAAGAACAATTGAAAAAACAATTAAAGGCATGCAAAACCAGTGAGAT 1019

Qy   849 cctgaagctgctcagtttgtgggaataacaatagagctcaaggctgaaggggcct 908
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1020 CCTGAAGCTGCTCAGTTTGTGGGAATAACAATAGAGCTCAAGGCTGAAGGGGCCT 1079

Qy   909 aatgcacgcactaaagcactcaagacgacgtaccacttcccaaaacgtcactcagagtct 968
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1080 AAATGCACGCACTAAAGCACTCAAGACGTACCACTTTCCCAAAAACGTCACTCAGAGTCT 1139

Qy   969 aaagaagaaccatcaggttcctccacagcttcacagccaatgtacaaaattgtatcacaagttatt 1028
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Db   1140 AAAGAAGAACCATCAGGTTCCTTCCACAGCTTCACAGCCACCACTTTCCCAAAAACGTCACTCAGAGTATT 1199

Qy   1029 tttagaaaatgatgataggtaaccagtccaatcagtaaaaataagctgcttataa 1080
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1200 TTTAGAAAATGATAGGTAACCAGTCCAATCAGTAAAAAATAAGCTGCTTATAA 1251
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CC   prevention of disorders of bone resorption, e.g. osteoporosis.
SQ   Sequence    984 BP;    313 A;    236 C;    212 G;    223 T;

Query Match      53.4%;    Score 816;    DB 27;    Length 984;
Best Local Similarity   99.9%;    Pred. No. 0.00e+00;
Matches    817;    Conservative    0;    Mismatches    1;    Indels    0;    Gaps    0;

Db     1 atgaacaacttgctctgtgtctgcgcgcctcgtgtttctggacatctccattaagtggaccacc   60
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Qy    46 ATGAACAAGTTGCTGTGCGTGCGCGCCTCGTGTTTCTGGACAATCTCCATTAAGTGGACCACC  105

Db    61 caggaaacgtttcctccaaagtacctcattattggcg...                         120
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Qy   106 CAGGAAACGTTTCCTCCAAAGTACCTCATTATGACGAAGAAACCTCTCATTAAGTGGACCACG  165

Db   121 tgtgaacaaatgtctcctcggtacctacacca...                              180
Qy   166 TGTGACAAATGTCCTCCTCGGTACCTACAAAACAACACTGTACAGCAAAGTGGAAGACC      225

Db   181 gtgtgtcgcgcccccttgccctgaccactactacaca...                         240
Qy   226 GTGTGTCGCGCCCCCTTGCCCTGACCACTACTACACAGACAGCAGGAGTCGAGTGT         285

Db   241 ctatactgcagccccggtgtccaaggagctcaagcta...                         300
Qy   286 CTATACTGCAGCCCCGGTGTCCAAGGAGCTCCAGTACTTCAAGACGTCGAGTCC          345

Db   301 cacaaaccggtgtccaaggagaaggcgcgctacactc...                         360
Qy   346 CACAAACCGGTGTCCAAGGAGAAGGCGCGCTACCTTGAGATAGAGTTCTGCTTGAAA        405

Db   361 cataggagctgccctcctggatttggagttgtgtcaa...                         420
Qy   406 CATAGGAGCTGCCCTCCTGGATTTGGAGTTGTGTCAAGTGGAAGCGTGGGAAATACA        465

Db   421 gtttgcaaaagatgtccagatgtggttcctcatcatc...                         480
Qy   466 GTTTGCAAAAGATGTCCAGATGGGTTCTTCTCAAATGAGACGTCATCTAAAGCACCCTGT     525

Db   481 agaaaaacacacaaaattgcagtgtcttgttctctcc...                         540
Qy   526 AGAAAACACACAAAATTGCAGTGTCTTGTTCTCTCCAGAAAGGAAATGCAACA           585

Db   541 cacgacaacatatgttccggaaacagtgaatcaactc...                         600
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Db   601 ctgtgtgaggagggcattcttcaaggtttgcttccta...                         660
Qy   646 CTGTGTGAGGAGGGCATTCTTCAGGTTTGCTTCCTACTACAAAGTTTACGGCTTAACTGGCTT  705

Db   661 agtgtcttggttagcacaaattgcctggcacacaaag...                         720
Qy   706 AGTGTCTTGGTTAGCACAAATTGCCTGGCACAAGTAAAGCAGAGAGTGTAGAGGGATA       765

Db   721 aaacggcaacacacgctcacagaacaagacttccag...                          780
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Db   781 aacaaagaccaaagatatagtcaagaagaatcatccaaga                         818
Qy   826 AACAAAGACCAAGAGAATAATAGTCAAGAAGAATCATCCAAGA                      863
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FT   /*tag=  b
FT   /product= OCIF-CDD2
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CC   DNA encoding osteoclastogenesis inhibitory factor protein - useful
PT   for bone resorption control, esp. treatment of osteoporosis
PS   Claim 66;  Page 145;  183pp; Japanese.
CC   This sequence encodes a mutated version of the full length
CC   osteoclastogenesis inhibitory factor (OCIF) of the invention. This
CC   sequence encodes OCIF-CDD2 in which amino acids 252-380 of the mature
CC   protein have been deleted. The OCIF of the invention has a molecular
CC   weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under
CC   non-reducing conditions. The protein is adsorbed onto cation-exchangers
CC   or heparin and its activity is lowered after 10 mins at 70 deg.C or 30
CC   mins at 56 deg.C, and is lost after 10 mins at 90 deg.C.  OCIF is useful
CC   in the control of bone resorption and therefore in the treatment and
CC   prevention of disorders of bone resorption, e.g. osteoporosis.
SQ   Sequence   819 BP;   251 A;   188 G;   182 T;

Query Match      53.3%;    Score 814;    DB 27;    Length 819;
Best Local Similarity   99.9%;    Pred. No. 0.00e+00;
Matches    815;    Conservative    0;    Mismatches    1;    Indels    0;    Gaps    0;

Db     1 atgaacaacttgctctgtgtctgcgcgcctcgtgtttctggacatctccattaagtggaccacc   60
Qy    46 ATGAACAAGTTGCTGTGCGTGCGCGCCTCGTGTTTCTGGACAATCTCCATTAAGTGGACCACC  105

Db    61 caggaaacgtttcctccaaagtacctcattattggcg...                         120
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Db   181 gtgtgtcgcgcccccttgccctgaccactactacaca...                         240
Qy   226 GTGTGTCGCGCCCCCTTGCCCTGACCACTACTACACAGACAGCAGGAGTCGAGTGT         285

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Qy   406 CATAGGAGCTGCCCTCCTGGATTTGGAGTTGTGTCAAGTGGAAGCGTGGGAAATACA        465

Db   421 gtttgcaaaagatgtccagatgtggttcctcatcatc...                         480
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Qy   526 AGAAAACACACAAAATTGCAGTGTCTTGTTCTCTCCAGAAAGGAAATGCAACA           585

Db   541 cacgacaacatatgttccggaaacagtgaatcaactc...                         600
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RESULT  14
ID   T33174 standard; DNA; 819 BP.
AC   T33174;
DT   22-APR-1997  (first entry)
DE   Mutated OCIF, OCIF-CDD2, coding sequence.
KW   Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
OS   osteoporosis; ss.
KW   Synthetic.
FH   Key            Location/Qualifiers
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CC   (SNOW )  SNOW BRAND MILK PROD CO LTD.
PA   Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
PI   Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
WPI; 96-403320/40.
PN   WO9626217-A1.
PD   29-AUG-1996.
PF   20-FEB-1996; J00374.
PR   20-FEB-1995; JP-054977.
PR   21-JUL-1995; JP-207508.
DR   P-PSDB; R99944.
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Db    601  ctgtgtgaggaggcaggcattcttcaggtttgctgttcttcctacaaagtttacgcctaactggctt  660
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Qy    646  CTGTGTGAGGAGGCAGGCATTCTTCAGGTTTGCTGTTCTTCCTACAAAGTTTACGCCTAACTGGCTT  705

Db    661  agtgtcttgtagacaacaatttgcctggcaccaaaagtaaacgcagagagagtagagaggata  720
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Qy    706  AGTGTCTTGTAGACAACAATTTGCCTGGCACCAAAAGTAAACGCAGAGAGAGTAGAGAGGATA  765

Db    721  aaacggcaacacagtctcacaagaacagacagtcttccacgctgctgaagtttatggaaacatcaa  780
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Qy    766  AAACGGCAACACAGCTCACAAGAACAGACAGTTTCCAGCTGCTGAAGTTTATGGAAACATCAA  834

Db    781  aacaaagaccaagatatagtcaagaagaagatcatccaa  816
           |||||||||||||||||||||||||||||||||||||||
Qy    826  AACAAAGACCAAGATATAGTCAAGAAGAAGATCATCCAA  861
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Query Match       50.18;   Score 765;   DB 27;   Length 1080;
Best Local Similarity 100.0%;   Pred. No. 0.00e+00;
Matches  765;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;
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Db    316  agagtccagatggggttcctccaaatgagacgtcatctctgaaagaaccacctgtagaaaacac  375
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Qy    475  AGAGTCCAGATGGGGTTCTTCTCAAATGAGACGTCATCTCTGAAAGAACCACCCTGTAGAAAACAC  534

Db    376  acaaattgcagtgtctttgtctcctgctaactcagaaagtgaacacacgacaac  435
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Qy    535  ACAAATTGCAGTGTCTTTGTCTCCTGCTAACTCAGAAAGTGAACACACGACAAC  594

Db    436  atatgttccggaaacacagtgaatcaactcaaaaaatgtggaatatagatgttacccctgtgtgag  495
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    595  ATATGTTCCGGAAACACAGTGAATCAACTCAAAAAATGTGGAATATAGATGTTACCCTGTGTGAG  654
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Db    496  gaggcaattcttcaggtttgctgttcttcctacaaagtttacgcctaactggctttagtgtcttg  555
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    655  GAGGCAATTCTTCAGGTTTGCTGTTCTTCCTACAAAGTTTACGCCTAACTGGCTTTAGTGTCTTG  714

Db    556  gtagacaatttgcctggcaccaaaagtaaacgcagagagagtagagaggataaaacggcaa  615
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Qy    715  GTAGACAATTTGCCTGGCACCAAAAGTAAACGCAGAGAGAGTAGAGAGGATAAAACGGCAA  774

Db    616  cacagtctcacaagaacagacagtcttccagctgctgaagtttatggaaacatcaaaacaaagac  675
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Qy    775  CACAGTCTCACAAGAACAGACAGTTTCCAGCTGCTGAAGTTTATGGAAACATCAAAACAAAGAC  834

Db    676  caagatatagtcaagaagaagatcatccaagatattgacctctgtgaaaacagcgtgcagcgg  735
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Qy    835  CAAGATATAGTCAAGAAGAAGATCATCCAAGATATTGACCTCTGTGAAAACAGCGTGCAGCGG  894

Db    736  cacattggacatgctaacctcaacctttcgagcagccagttcgtttgatcttgatggaaagcttac  795
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Qy    895  CACATTGGACATGCTAACCTCAACCTTTCGAGCAGCCAGTTCGTTTGATCTTGATGGAAAGCTTACG  954

Db    796  ggaaagaaagtcgggagcagatcgaaaaaacaatcaaagccatgcaccagtcggcaaccccagtcac  855
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Qy    955  GGAAAGAAAGTGGGAGCAGAGACGAAGACACATTGAAAAAACAATAAAAGCCATGCAGCAGTGAC  1014

Db    856  cagatcctgaagctgtccagtttgtggcgaataaaaatggcggaccaagcacacctttgaag  915
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Db    916  ggcctaatgcacgcacactaaaagacactcaaagaagtatacaccttttcccaaaaactgtcaactcag  975
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Db    976  agtcctaaagaagagaccatcaaggtttccttcacagcgttcaccaatgttacaaattgtatcagaag  1035
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Qy    1135 AGTCTAAAGAAGAGACCATCAAGGTTTCCTTCACAGCGTTCACCAATGTTACAAATTGTATCAGAAG  1194

Db    1036 ttattttagaaatgataggtaaccaggtccaatccagtaaaaata  1080
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